



**Fig. 2a**

[illegible]

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Fig. 2b

380 390 400 410 420 430 440  
 a: GACATGTATCTCAGCCCTGTTGCCATGTTTCGGGACCCCTTCGCGCAGAGATCCCAACAAGCTGGTCTGTGAA  
 b: D M Y L S P V A M F R D P F R R D P N K L V P C E  
 c: M Y L V P a A M F R D P F k R D P N X L V P C E  
 d: CB XII-C CB VI-C  
 75 80 85 90 95

450 460 470 480 490 500 510 520  
 a: GTTTTCAAGTACAACCGGAGCCTGCCAGAGACCAATTTAAGGCACCTCGTGTAACGGATAATGGACATGGTGAGC  
 b: V F K Y N R K P A E T N L R H S C K R I M D M V S  
 c: V F X Y N k r P A E T N L X X t C  
 d: CB XIV CB XII-C  
 100 105 110 115 120

530 540 550 560 570 580 590  
 a: AACGAGACCCCTGTTTGGAAATGGAACAGGAGTACTCTGATGGGAACAGATGGGCACCCCTTTTGGTTGGCCT  
 b: N Q H P W F G M E Q E Y T L M G T D G H P P G W P  
 c: N Q X P P X F G M E Q E Y T L M G T r G r P P G X P  
 d: CB XII-A CB VI-D  
 125 130 135 140 145

600 610 620 630 640 650 660 670  
 a: TCCAAATGGCTTTCCTGGGCCCAAGTCCGTATTACTGTGGTGGCGCAGACAAAGCCATGGCAGGATATC  
 b: S N G F P G P Q G P Y Y C G V G A D K A Y G R D I  
 c: S N C F X G P Q a  
 150 155 160 165 170

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Fig. 2c

680 690 700 710 720 730 740  
 a: CTGGAGGCTCACTACCGCGCTGCTTGTATGCTGGGTCAAGATTACAGGAACAAATGCTGAGTCAATGCCTGCC  
 b: V E A H Y R A C L Y A G V K I T G T N A E V M P A  
 c: A C L Y A G i K g G T N X X V M P A  
 d: T VII-G 180 185 190 195 CB XI-H  
 175

750 760 770 780 790 800 810 820  
 a: CAGTGGGAATTCCAAATAGGACCCCTGTGAAGGAATCCGCATGGGAGATCATCTCTGGGTGGCCCGTTTCATCTTG  
 b: Q W E F Q I G P C E G I R M G D H L W V A R F I L  
 c: Q W E F Q I G P C E G I d M 215 220  
 200 205 210

830 840 850 860 870 880 890  
 a: CATCGAGTATGTGAAGACTTTGGGGTAATAGCAACCTTTGACCCCAAGCCCATCTCTGGGAACCTGGAAATGGTGCA  
 b: H R V C E D F G V I A T F D P K P I P G N W N G A  
 225 230 235 240 245

900 910 920 930 940 950 960 970  
 a: GGCTGCCATACCAACTTTAGCACCAAGGCCATGCGGGAGGAGAAATGGTCTGAAGCACATCGAGGAGGCCATCGAG  
 b: G C H T N F S T K A M R E E N G L K H I E E A I E  
 c: M X E E N G L K Y I E E A I E  
 d: CB III-C 255 260 265 270  
 250

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**Fig. 2d**

	1200	1210	1220	1230	1240	1250	1260	1270
a:	GTGACAGAGCCATCGTCCGCACATGCCCTTCTCAATGAGACTGGCGCAGAGCCCTTCCAAATACAAAACCTAATTA							
b:	V T E A I V R T C L L N E T G D E P P Q Y K N ***							
c:			T C L L N Z T G B Z P P Q Y K					
d:	350	355	T VI-K		360	365	370	372

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1280 1290 1300 1310 1320 1330 1340  
a: GACTTTGAGTGATCTTGAGCCCTTCCCTAGTTCATCCACCCCGCCCGCTGTCTCATTTGTAACTCAAAGGATGG

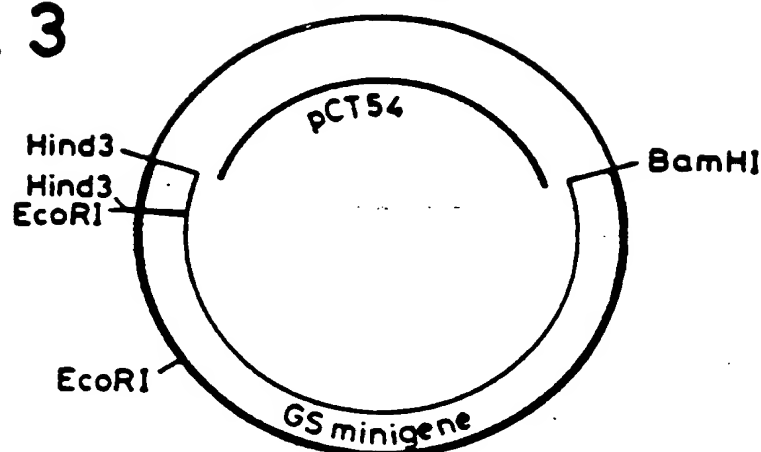
1350 1360 1370 1380 1390 1400 1410 1420  
a: AATATCAAGGTCCTTTTATTCCCTCGTGCCAGTTAATCTTGCTTTTATTGGTCAGAAATAGAGGAGTCAAGTTCTT  
c: AATATCAAGGTCCTTTTATTCCCTCGTGCCCAAAAAAAAAAAAAAAAAAAAAAAAAA

Fig. 2e

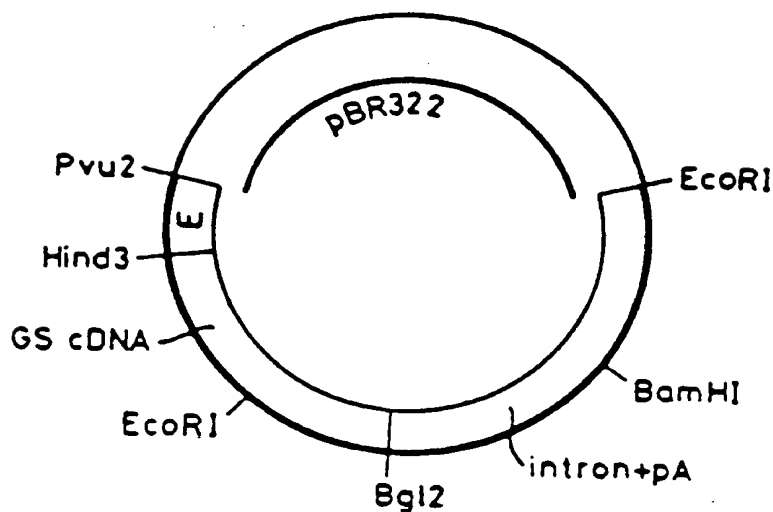
Fig. 3

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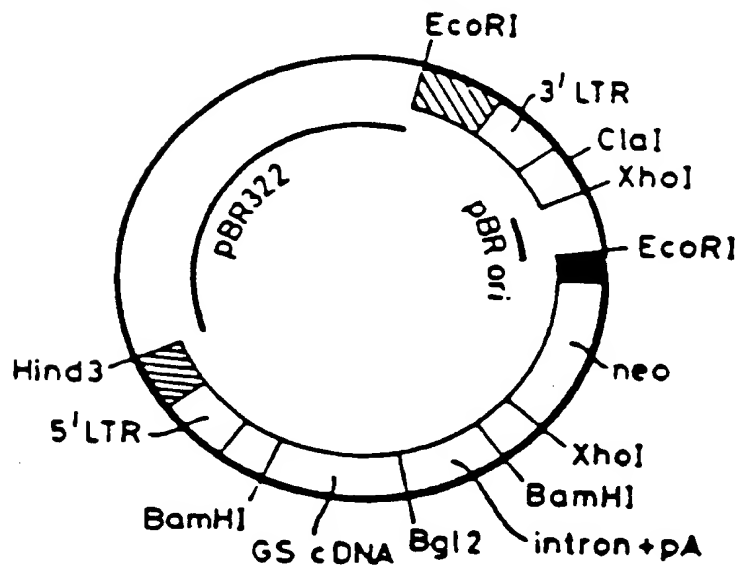
a) pSVLGS.1



b) pSV2.GS



c) pZIPGS



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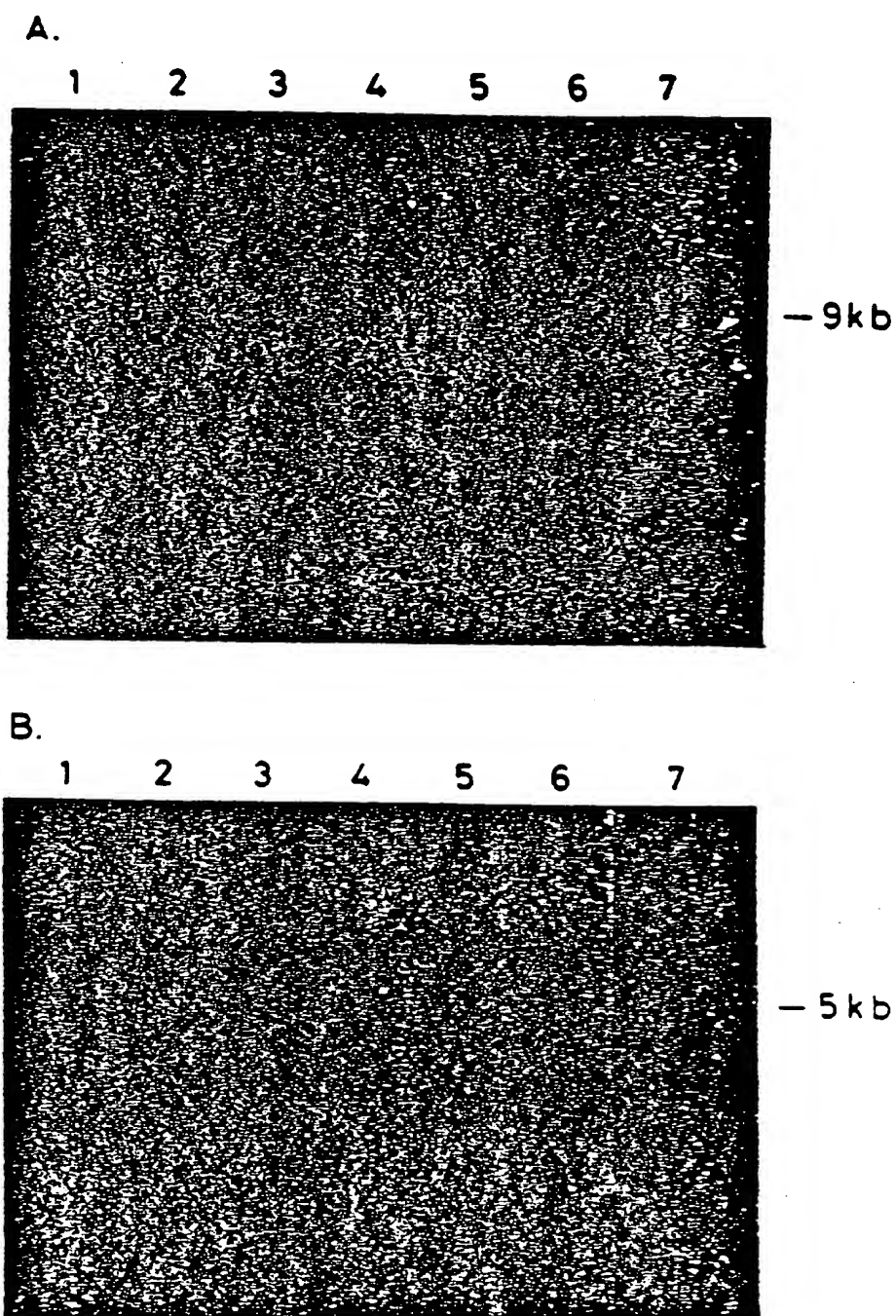


Fig. 4



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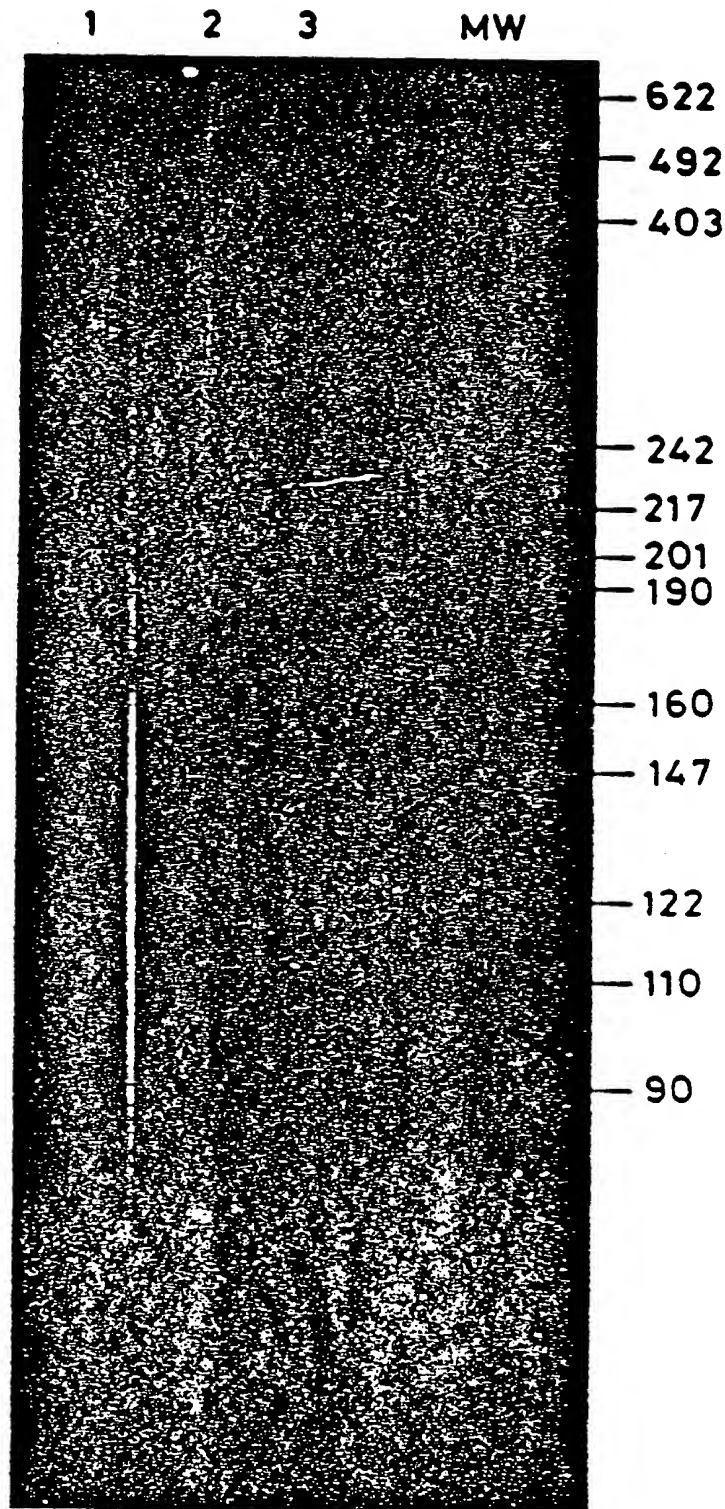


Fig. 5